

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Limits

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History

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Details

Show:

☐ 1: AAA28373. Antennepedia prot...[gi:156934]

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LOCUS AAA28373 74 aa linear INV 26-APR-1993

DEFINITION Antennepedia protein.

ACCESSION AAA28373

VERSION AAA28373.1 GI:156934

DBSOURCE locus DROANTC2 accession [K01948.1](#)

KEYWORDS .

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM [Drosophila melanogaster](#)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (residues 1 to 74)

AUTHORS McGinnis,W., Garber,R.L., Wirz,J., Kuroiwa,A. and Gehring,W.J.

TITLE A homologous protein-coding sequence in Drosophila homeotic genes
and its conservation in other metazoans

JOURNAL Cell 37 (2), 403-408 (1984)

MEDLINE [84205674](#)

PUBMED [6327065](#)

COMMENT Method: conceptual translation.

FEATURES Location/Qualifiers

source 1..74
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/map="right arm of ch. 3"

Protein 1..74
/name="Antennepedia protein"

CDS 1..74
/coded_by="complement(K01948.1:<1..>222)"

ORIGIN

1 iylepterkr grqtytryqt lelekefhfn ryltrrrrie iahalclter qikiwfnrr
61 mkwkkenktk gepd

//


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Apr 24 2003 13:08:07

>gi|156934|gb|AAA28373.1| Antennepedia protein
Length = 74

Score = 61.7 bits (138), Expect = 1e-09
Identities = 16/16 (100%), Positives = 16/16 (100%)

Query: 1 RQIKIWFQNRRMKWKK 16
RQIKIWFQNRRMKWKK
Sbjct: 50 RQIKIWFQNRRMKWKK 65

	BLAST	Protein	Structure	PubMed	Taxonomy
	Genome	Nucleotide	3D-Domains	Books	Help

Query: gi|156934 Antennapedia protein













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 ☐ Fungi
 ☐ Plants
 ☐ 1 Viruses
 ☐ Other Eukaryotae

Keep only ☒ Cut-Off [Select](#) [Reset](#)

74 aa

	SCORE	P	ACCESSION	GI	PROTEIN DESCRIPTION
	362	20	AAC31945	3420836	Antennapedia homeotic protein [Anop
	362	19	BAA04087	391615	Antennapedia homologue protein [Bom
	362	35	A25399	84890	homeotic protein Antennapedia - fru
	362	34	AAO00997	27374237	Antp-PA [Drosophila erecta]
	362	20	EAA07256	21295111	agCP12956 [Anopheles gambiae str. P
	362	19	S58850	1363994	homeotic protein abd-A - Junonia co
	362	32	CAA43307	829192	Antp [Drosophila subobscura]
	357	31	AAA28737	158023	homeobox protein
	357	35	1HOM	443020	Chain , Antennapedia Protein (Home
	355	19	AAF69136	7767519	prothoraxless [Tribolium castaneum]
	355	19	AAK96031	15450324	homeodomain transcription factor Pr
	349	19	CAC06383	9967824	Antennapedia protein [Apis mellifer

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2003, 00:06:36 ; Search time 965 Seconds
(without alignments)
5971.353 Million cell updates/sec

Title: US-09-654-743-51
Perfect score: 198
Sequence: 1 tatgaagcagcgtcttac.....accacgggtgcaataaccta 198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
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- 28: em.un.*
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- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pln.*
- 35: em.htg_rtd.*
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- 38: em.sy.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	198	100.0	2100	6	AX412124 Sequence
2	194.8	98.4	2691	6	AR106400 Sequence
3	194.8	98.4	2691	6	AR116702 Sequence
4	194.8	98.4	2691	10	MMU88990 Mus musculus
5	186.8	94.3	1988	10	MMU36842 Mus musculus
6	182	91.9	1491	10	AF183429 Rattus no
7	182	91.9	2468	10	AB033366 Rattus no
8	182	91.9	2032	10	AF304334 Rattus no
9	180.4	91.1	2032	10	AF304333 Rattus no
10	173	87.4	1659	6	E31042 Method for
11	173	87.4	1659	9	U32974 Human IAP-1
12	173	87.4	2086	9	BC032729 Homo sapi
13	173	87.4	2404	6	AX429575 Sequence
14	173	87.4	2540	6	AR103281 Sequence
15	173	87.4	2540	6	AX412118 Sequence
16	173	87.4	2540	9	HSU45880 Human X-lin
17	173	87.4	3000	6	AX412131 Sequence
18	173	87.4	5232	6	AR106397 Sequence
19	173	87.4	5232	6	AR116699 Sequence
20	157	79.3	1752	6	AX104956 Sequence
21	157	79.3	1752	9	AF164681 Homo sapi
22	157	79.3	154214	9	AC079753 Homo sapi
23	149	75.3	1758	6	AX370787 Sequence
24	149	75.3	1758	6	AX370789 Sequence
25	149	75.3	4993	6	AX104968 Sequence
26	149	75.3	4993	9	AF164682 Homo sapi
27	149	75.3	143401	9	AC010467 Homo sapi
28	149	75.3	165662	9	AC092070 Homo sapi
29	147.4	74.4	711	6	AR121220 Sequence
30	147.4	74.4	711	6	AR123871 Sequence
31	147.4	74.4	2032	9	AF420440 Homo sapi
32	145.8	73.6	711	6	AX104970 Sequence
33	145.8	73.6	711	9	AY030052 Pan trogl
34	144.2	72.8	711	6	AX104972 Sequence
35	144.2	72.8	711	9	AY030053 Gorilla g
36	131.6	66.5	187568	9	AP002967 Homo sapi
37	130	65.7	184439	2	AP003085 Homo sapi
38	121.4	61.3	327	4	AF458770 Bos tauru
39	104.2	52.6	1740	5	AF451854 Gallus ga
40	85.8	43.3	133391	9	HSJ31561 Human DNA
41	85.8	43.3	201197	2	HS424J12 Human DNA
42	77	38.9	1550	4	SSU79142 Homo sapien
43	76.6	38.7	158093	9	AL390123 Sus scrofa
44	76	38.4	2563	9	AL390123 Human DNA
45	76	38.4	2601	6	AR129833 Homo sapien

ALIGNMENTS

RESULT 1	AX412124	Sequence 224 from Patent WO0226968.	2100 bp	DNA	linear	RAT 15-JUN-2002
LOCUS	AX412124					
DEFINITION	Sequence 224 from Patent WO0226968.					
ACCESSION	AX412124					
VERSION	AX412124.1	GI:21444584				
KEYWORDS	house mouse					
SOURCE	house mouse					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Mus.					
TITLE	Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.					
JOURNAL	Antisense lrp nucleic acids and uses thereof					
	Patent: WO 0226968-A 224 04-APR-2002;					

University of Ottawa (CA) : Aegera Therapeutics Inc. (CA)

FEATURES
Source
1..2100
/organism="Mus musculus"
/db_xref="taxon:10090"

BASE COUNT 615 a 417 c 482 g 586 t
ORIGIN

Query Match 100.0%; Score 198; DB 6; Length 2100;
Best Local Similarity 100.0%; Pred. No. 7.1e-46;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 916 TATGAGCAGCGATCGTTACTTTTGGACATGATATCTACTGTTAAACAGGAGCAGCTT 975
|||||

QY 61 GCAAGAGCTGGATTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 120
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Db 976 GCAAGAGCTGGATTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 1035
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QY 121 GGAGGCTCAGCGATTGGAAGCAAGTGAAGCCCTGGACAGCATGCTAAGTCTCTAC 180
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Db 1036 GGAGGCTCAGCGATTGGAAGCAAGTGAAGCCCTGGACAGCATGCTAAGTCTCTAC 1095
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QY 181 CCAGGTGCAAAATACCTA 198
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Db 1096 CCAGGTGCAAAATACCTA 1113
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RESULT 2
LOCUS AR106400 2691 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6107041.
ACCESSION AR106400
VERSION AR106400.1 GI:12820930
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.
TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease
JOURNAL Patent: US 6107041-A 9 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..2691
BASE COUNT 819 a 479 c 562 g 831 t
ORIGIN

Query Match 98.4%; Score 194.8; DB 6; Length 2691;
Best Local Similarity 99.0%; Pred. No. 5.5e-45;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTACTGTTAAACAGGAGCAGCTT 60
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Db 1461 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTACTGTTAAACAGGAGCAGCTT 1520
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QY 61 GCAAGAGCTGGATTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 120
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Db 1521 GCAAGAGCTGGATTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 1580
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QY 121 GGAGGCTCAGCGATTGGAAGCAAGTGAAGCCCTGGACAGCATGCTAAGTCTCTAC 180
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Db 1581 GGAGGCTCAGCGATTGGAAGCAAGTGAAGCCCTGGACAGCATGCTAAGTCTCTAC 1640
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QY 181 CCAGGTGCAAAATACCTA 198
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Db 1641 CCAGGTGCAAAATACCTA 1658
|||||

RESULT 3
LOCUS AR106400 2691 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6107041.
ACCESSION AR106400
VERSION AR106400.1 GI:12820930
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.
TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease
JOURNAL Patent: US 6107041-A 9 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..2691
BASE COUNT 819 a 479 c 562 g 831 t
ORIGIN

Query Match 98.4%; Score 194.8; DB 6; Length 2691;
Best Local Similarity 99.0%; Pred. No. 5.5e-45;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1461 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTACTGTTAAACAGGAGCAGCTT 1520
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QY 61 GCAAGAGCTGGATTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 120
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Db 1521 GCAAGAGCTGGATTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 1580
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QY 121 GGAGGCTCAGCGATTGGAAGCAAGTGAAGCCCTGGACAGCATGCTAAGTCTCTAC 180
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Db 1581 GGAGGCTCAGCGATTGGAAGCAAGTGAAGCCCTGGACAGCATGCTAAGTCTCTAC 1640
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QY 181 CCAGGTGCAAAATACCTA 198
|||||
Db 1641 CCAGGTGCAAAATACCTA 1658
|||||

AR116702 2691 bp DNA linear PAT 16-MAY-2001
LOCUS AR116702
DEFINITION Sequence 9 from patent US 6133437.
ACCESSION AR116702
VERSION AR116702.1 GI:14097024
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.
TITLE Modulation of IAPs for the treatment of proliferative diseases
JOURNAL Patent: US 6133437-A 9 17-OCT-2000;
FEATURES Location/Qualifiers
source 1..2691
BASE COUNT 819 a 479 c 562 g 831 t
ORIGIN

Query Match 98.4%; Score 194.8; DB 6; Length 2691;
Best Local Similarity 99.0%; Pred. No. 5.5e-45;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 GCAAGAGCTGGATTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 120
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Db 1521 GCAAGAGCTGGATTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 1580
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QY 121 GGAGGCTCAGCGATTGGAAGCAAGTGAAGCCCTGGACAGCATGCTAAGTCTCTAC 180
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Db 1581 GGAGGCTCAGCGATTGGAAGCAAGTGAAGCCCTGGACAGCATGCTAAGTCTCTAC 1640
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QY 181 CCAGGTGCAAAATACCTA 198
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Db 1641 CCAGGTGCAAAATACCTA 1658
|||||

RESULT 4
LOCUS MMU88990 2691 bp mRNA linear ROD 31-MAY-1997
DEFINITION Mus musculus X-linked inhibitor of apoptosis (miap-3) mRNA, complete cds.
ACCESSION U88990
VERSION U88990.1 GI:2138318
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.
TITLE Genomic Organization and Primary Characterization of miap-3: The Murine Homologue of Human X-Linked IAP
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2691)
AUTHORS Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-1997) Molecular Genetics, Children's Hospital of Eastern Ontario, 401 Smyth Rd., Ottawa, Ontario K1H 8L1, Canada
FEATURES Location/Qualifiers
source 1..2691
BASE COUNT 819 a 479 c 562 g 831 t
ORIGIN

Query Match 98.4%; Score 194.8; DB 6; Length 2691;
Best Local Similarity 99.0%; Pred. No. 5.5e-45;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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|||||

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QY 121 GGAGGCTCAGCGATTGGAAGCAAGTGAAGCCCTGGACAGCATGCTAAGTCTCTAC 180
|||||
Db 1581 GGAGGCTCAGCGATTGGAAGCAAGTGAAGCCCTGGACAGCATGCTAAGTCTCTAC 1640
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QY 181 CCAGGTGCAAAATACCTA 198
|||||
Db 1641 CCAGGTGCAAAATACCTA 1658
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RESULT 5
LOCUS MMU88990 2691 bp mRNA linear ROD 31-MAY-1997
DEFINITION Mus musculus X-linked inhibitor of apoptosis (miap-3) mRNA, complete cds.
ACCESSION U88990
VERSION U88990.1 GI:2138318
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.
TITLE Genomic Organization and Primary Characterization of miap-3: The Murine Homologue of Human X-Linked IAP
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2691)
AUTHORS Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-1997) Molecular Genetics, Children's Hospital of Eastern Ontario, 401 Smyth Rd., Ottawa, Ontario K1H 8L1, Canada
FEATURES Location/Qualifiers
source 1..2691
BASE COUNT 819 a 479 c 562 g 831 t
ORIGIN

Query Match 98.4%; Score 194.8; DB 6; Length 2691;
Best Local Similarity 99.0%; Pred. No. 5.5e-45;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 GCAAGAGCTGGATTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 120
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Db 1521 GCAAGAGCTGGATTATGCTTTAGTGAAGCGGATAAAGTGAAGTCCACTGTGGA 1580
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QY 121 GGAGGCTCAGCGATTGGAAGCAAGTGAAGCCCTGGACAGCATGCTAAGTCTCTAC 180
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QY 181 CCAGGTGCAAAATACCTA 198
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Db 1641 CCAGGTGCAAAATACCTA 1658
|||||

Rattus.		Lareu, R.R., Bradley, C.K., Lacher, M., Friis, R.R. and Dharmarajan, A.M.		TITLE		Cloning, characterization and regulation of an inhibitor of apoptosis protein in the rat corpus luteum		JOURNAL		Unpublished		REFERENCE		2 (bases 1 to 3032)		AUTHORS		Lareu, R.R., Lacher, M., Friis, R.R. and Dharmarajan, A.M.		TITLE		Direct Submission		JOURNAL		Submitted (08-SEP-2000) Anatomy and Human Biology, University of Western Australia, Verduin St, Nedlands, WA 6907, Australia		FEATURES		Location/Qualifiers		source																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
		1. .3032				/organism="Rattus norvegicus"		/strain="Wistar"		/db_xref="taxon:10116"		/clone="2"		/tissue_type="ovary"		/note="isolated at day 15 of pregnancy"		926. .2431		/note="IAP3"		/codon_start=1		/product="inhibitor of apoptosis protein 3"		/protein_id="AAG41193.1"		/db_xref="GI:11890721"		/translation="MTFNSFEGSTVVPADTKDEEFVEENRLKTFANFPSSSPVSA		STLARAGLTYTGEQDTVQCFSCHAADVDRWQYSDSAVGRHRRISPNCRFINGRFYFENGA		TQSTSPGQNGQYKSENCVGRNHRFALDRPSETHADYLLRTGQVVDISDTIYPRNPAM		CSEARLKTQNFWDYAHLSPRELASGLYITGIDQVQCFCCGKLNWPCDRAWS		EHRHFFPCFVLGRNVNRSVSGSSDORFNPNSTNPRNPAEYDARIYTFGTWLY		SVNKEQLARAGFYALGEGDKVKCPHGGGLDWKPSDPEQWQHAQYPCGYLLDEKG		QYINNIHLTHSLGESVVRTEAKTPSVTKKIDDTIFQNPVQEAIRMGFNPKDILKKT		BEKLTQSSNVLSEVLADLVSAQKNSQDESSQTSLOKDI STEQRLRQEEKLK		ICMORNIATVFPVGHLYTKQCAEAVDKCPMCCTVITFKQKFLCLNPAQ"																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
BASE COUNT		817 a 657 c 688 g 870 t		ORIGIN		Query Match		91.9%; Score 182; DB 10; Length 3032;		Best Local Similarity		94.9%; Pred. No. 2.4e-41;		Matches 188; Conservative		0; Mismatches 10; Indels		0; Gaps		0;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY		1		TATGAAGCAGGATCTTACTTTTGGACATGATATCTACATGATTAACAGGAGCAGCTT		60				DB		1715		TATGAGCAGGATCTTACTTTTGGACATGATATCTACATGATTAACAGGAGCAGCTT		1774				QY		61		GCAAGAGCTGGATTTATGCTTTAGTGAAGGGGATAAAGTGAAGTCTTCCACTGTGA		120				DB		1775		GCAAGAGCTGGATTTATGCTTTAGTGAAGGGGATAAAGTGAAGTCTTCCACTGTGA		1834				QY		121		GGAGGCTCAGGATTTAGTGAAGGGGATAAAGTGAAGGGGATAAAGTGAAGTCTTCCACTGTGA		180				DB		1835		GGAGGCTCAGGATTTAGTGAAGGGGATAAAGTGAAGGGGATAAAGTGAAGTCTTCCACTGTGA		1894				QY		181		CCAGGCTCAATATACCTA		198				DB		1895		CCAGGCTCAATATACCTA		1912																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
RESULT 9		AF304333		LOCUS		AF304333		DEFINITION		Rattus norvegicus clone 1 inhibitor of apoptosis protein 3 mRNA, complete cds.		ACCESSION		AF304333		VERSION		AF304333.1		GI:11890718		SOURCE		Rattus norvegicus.		ORGANISM		Rattus norvegicus.		REFERENCE		1 (bases 1 to 2032)		AUTHORS		Lareu, R.R., Lacher, M., Friis, R.R. and Dharmarajan, A.M.		TITLE		Cloning, characterization and regulation of an inhibitor of apoptosis protein in the rat corpus luteum		JOURNAL		Unpublished		REFERENCE		2 (bases 1 to 2032)		AUTHORS		Lareu, R.R., Lacher, M., Friis, R.R. and Dharmarajan, A.M.		TITLE		Direct Submission		JOURNAL		Submitted (08-SEP-2000) Anatomy and Human Biology, University of Western Australia, Verduin St, Nedlands, WA 6907, Australia		FEATURES		Location/Qualifiers		source																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
		1. .2032				/organism="Rattus norvegicus"		/strain="Wistar"		/db_xref="taxon:10116"		/clone="1"		/tissue_type="ovary"		/note="isolated at day 15 of pregnancy"		125. .1630		/note="IAP3"		/codon_start=1		/product="inhibitor of apoptosis protein 3"		/protein_id="AAG41192.1"		/db_xref="GI:11890719"		/translation="MTFNSFEGSTVVPADTKDEEFVEENRLKTFANFPSSSPVSA		STLARAGLTYTGEQDTVQCFSCHAADVDRWQYSDSAVGRHRRISPNCRFINGRFYFENGA		TQSTSPGQNGQYKSENCVGRNHRFALDRPSETHADYLLRTGQVVDISDTIYPRNPAM		CSEARLKTQNFWDYAHLSPRELASGLYITGIDQVQCFCCGKLNWPCDRAWS		EHRHFFPCFVLGRNVNRSVSGSSDORFNPNSTNPRNPAEYDARIYTFGTWLY		SVNKEQLARAGFYALGEGDKVKCPHGGGLDWKPSDPEQWQHAQYPCGYLLDEKG		QYINNIHLTHSLGESVVRTEAKTPSVTKKIDDTIFQNPVQEAIRMGFNPKDILKKT		BEKLTQSSNVLSEVLADLVSAQKNSQDESSQTSLOKDI STEQRLRQEEKLK		ICMORNIATVFPVGHLYTKQCAEAVDKCPMCCTVITFKQKFLCLNPAQ"																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
BASE COUNT		609 a 385 c 473 g 565 t		ORIGIN		Query Match		91.1%; Score 180.4; DB 10; Length 2032;		Best Local Similarity		94.4%; Pred. No. 7.2e-41;		Matches 187; Conservative		0; Mismatches 11; Indels		0; Gaps		0;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Contact: nisc.mcgenhri.nih.gov
 Web site: http://www.nisc.nih.gov/
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granice, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Series: IRAK Name: 69 Row: 1 Column: 18
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4502142.

FEATURES

Location/Qualifiers

1..2086

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 /clone="MGC:45369 IMAGE:5532247"
 /tissue_type="Uterus, leiomyosarcoma"
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 /note="vector: pCMV-SPORT6"
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CDS

/codon_start=1
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 /protein_id="AAH32729.1"
 /db_xref="GI:21619764"
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 TSTNSGQNGQTKVENVYLGSRDFALDRPSETHADYLLRTGTGVVDSDIYPRNPAM
 YSEEARLKSGFNWPDYAHLPRELASAGLYITGIDVQVCFCCGKLNWPCDRAMS
 EHRHPNCFVILGRNLNIRSEDAVSDDNFPNPNLPPNSMADYEARIFFTGTWI
 YSVNKLQALRAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQAKWYPCGKYLLEQK
 GORYINHLTHSLRECLVETTEKTPSLTRIDDTIFONPMVOEALRMGFSFKDIIKI
 MEKTOISGNSVKSLEVLADLVNAOKDSQDRESSOTSLOKELSTEQRLRLQELCLC
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 689 a 341 c 450 g 606 t

BASE COUNT

ORIGIN

Query Match 87.4%; Score 173; DB 9; Length 2086;
 Best Local Similarity 92.4%; Pred. No. 9.1e-39;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAACACGGATCGTTACTTTTGGACATGGATATCTACTAGTTACAGAGGACAGCTT 60
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 Db 871 TATGAACACGGATCGTTACTTTTGGACATGGATATCTACTAGTTACAGAGGACAGCTT 930
 QY 61 GCAGAGCTGGATTTATGCTTTAGGTGAAGCGCATTAAGTGAAGTCTCCACTGTGGA 120
 |||||
 Db 931 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGCATTAAGTGAAGTCTTCACGTGTGA 990
 QY 121 GGAGGGCTCAGCGGATTTGAAGCGCATTAAGCGCCCTGGGACAGCATGCTTAAGTGTCTAC 180
 |||||
 Db 991 GGAGGGCTACTGATTTGAAGCGCCCTGGGACAGCATGCTTAAGTGTCTAC 1050
 QY 181 CCAGGGTGCAAAATACCT 197
 |||||
 Db 1051 CCAGGGTGCAAAATATCT 1067

RESULT 13
 AX429575
 LOCUS
 DEFINITION Sequence 38 from Patent WO0226820.
 2404 bp DNA linear PAT 21-JUN-2002

ACCESSION AX429575
 VERSION AX429575.1 GI:21540833
 KEYWORDS human.
 SOURCE Homo sapiens

REFERENCE 1
 AUTHORS Cohen, D., Dengler, U.J., Pinelli, A.L., Freuler, F., Konsolaki, M.,
 Reinhardt, M.W. and Zusman, S.
 TITLE Transgenic drosophila melanogaster expressing beta amyloid
 JOURNAL Patent: WO 0226820-A 38 04-APR-2002;
 NOVARTIS ERFINO VERWALT GMBH (AT)
 FEATURES Location/Qualifiers
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 source /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 759 a 372 c 525 g 748 t
 ORIGIN

Query Match 87.4%; Score 173; DB 6; Length 2404;
 Best Local Similarity 92.4%; Pred. No. 8.9e-39;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAACACGGATCGTTACTTTTGGACATGGATATCTACTAGTTACAGAGGACAGCTT 60
 |||||
 Db 827 TATGAACACGGATCGTTACTTTTGGACATGGATATCTACTAGTTACAGAGGACAGCTT 886
 QY 61 GCAGAGCTGGATTTATGCTTTAGGTGAAGCGCATTAAGTGAAGTCTCCACTGTGGA 120
 |||||
 Db 887 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGCATTAAGTGAAGTCTTCACGTGTGGA 946
 QY 121 GGAGGGCTCAGCGGATTTGAAGCGCATTAAGCGCCCTGGGACAGCATGCTTAAGTGTCTAC 180
 |||||
 Db 947 GGAGGGCTAACTGATTTGAAGCGCCCTGGGACAGCATGCTTAAGTGTCTAC 1006
 QY 181 CCAGGGTGCAAAATACCT 197
 |||||
 Db 1007 CCAGGGTGCAAAATATCT 1023

RESULT 14
 LOCUS AR103281
 DEFINITION Sequence 1 from patent US 6087173.
 ACCESSION AR103281
 VERSION AR103281.1 GI:12814869
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 1 (bases 1 to 2540)
 AUTHORS Bennett, C. Frank., Ackermann, B.J. and Cowser, L.M.
 TITLE Antisense modulation of X-linked inhibitor of apoptosis expression
 JOURNAL Patent: US 6087173-A 11-JUL-2000;
 FEATURES Location/Qualifiers
 1..2540
 source /organism="unknown"
 BASE COUNT 781 a 415 c 571 g 773 t
 ORIGIN

Query Match 87.4%; Score 173; DB 6; Length 2540;
 Best Local Similarity 92.4%; Pred. No. 8.8e-39;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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 Db 826 TATGAACACGGATCGTTACTTTTGGACATGGATATCTACTAGTTACAGAGGACAGCTT 885
 QY 61 GCAGAGCTGGATTTATGCTTTAGGTGAAGCGCATTAAGTGAAGTCTCCACTGTGGA 120
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search completed: April 19, 2003, 02:09:21
Job time : 974 secs

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Result No.	Query %			Length	DB	ID	Description
	Score	Match					
1	198	100.0	2100	18	AAT70839	Mouse apoptosis in	
2	198	100.0	2100	24	ABK93872	Mouse cDNA encoding	
3	194.8	98.4	2691	19	AAV55041	Murine XIAP coding	
4	186.8	94.3	1988	18	AAT72710	Mouse inhibitor of	
5	173	87.4	1659	21	AAZ48862	Human XIAP coding	
6	173	87.4	2404	24	AAK99405	DNA of APP related	
7	173	87.4	2540	18	AAT70836	Human apoptosis in	
8	173	87.4	2540	21	AAAG4901	Human X-linked inh	
9	173	87.4	2540	24	ABK93869	Human cDNA encoding	

XX
PA (UYOT-) UNIV OTTAWA

XX Baird S, Korneluk RG, Liston P, Mackenzie AE;
PI WPI; 1997-154262/14.
XX P-PSDB; AAW19584.
XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
PT of susceptibility to apoptotic disease
XX
XX Claim 11; Page 78-79; 219pp; English.
XX Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and
CC hiap-2 genes (AA70836-41) respectively code for a new class of
CC mammalian proteins (AAW19581-86) that are inhibitors of apoptosis
CC (IAP). The murine xiap gene (for X-linked IAP gene) sequence was
CC constructed from 12 overlapping clones isolated from a mouse
CC embryo lambda-gt11 cDNA library and from a mouse FIX II genomic
CC library using human xiap cDNA as probe. IAP nucleic acids can be
CC used to express IAP polypeptides in cells and animals to inhibit
CC apoptosis, and as primers and probes to identify and isolate
CC additional IAP genes, as well as in methods for treating diseases
CC and disorders involving apoptosis (anti-apoptotic gene therapy).
XX
XX Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;
Query Match 100.0%; Score 198; DB 18; Length 2100;
Best Local Similarity 100.0%; Pred. No. 1.3e-58;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTACTAGTTAAACAGGAGCGCTT 60
DB 916 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTACTAGTTAAACAGGAGCGCTT 975
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTCCACTGTGA 120
DB 976 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTCCACTGTGA 1035
QY 121 GGAGGGCTCACGGATTGGAGCCCAAGTGAAGCCCTTGGACCGACGATCTTAAGTGCTAC 180
DB 1036 GGAGGGCTCACGGATTGGAGCCCAAGTGAAGCCCTTGGACCGACGATCTTAAGTGCTAC 1095
QY 181 CCAGGGTGCAAAATACCTA 198
DB 1096 CCAGGGTGCAAAATACCTA 1113
RESULT 2
ABK93872
ID ABK93872 standard; cDNA; 2100 BP.
XX
XX AC ABK93872;
XX
XX 26-AUG-2002 (first entry)
XX
XX Mouse cDNA encoding inhibitor of apoptosis, XIAP.
XX
XX Mouse; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KW pancreatic cancer; embryonic development; viral pathogenesis;
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KW lupus erythematosus; herpes virus infection; pox virus infection;
KW adenovirus infection; proliferative disease.
XX
XX Mus sp.
XX
XX WO200225968-A2.
XX
XX 04-APR-2002.
XX
XX 27-SEP-2001; 2001WO-CA01379.
XX
XX 28-SEP-2000; 2000US-0672717.

XX (UYOT-) UNIV OTTAWA
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX WPI; 2002-479562/51.
XX P-PSDB; ABG55665.
XX Novel antisense inhibitor of apoptosis nucleic acid useful for
PT enhancing apoptosis in a cell, for treating cancer and other
PT proliferative diseases
XX
XX Disclosure; Fig 4; 135pp; English.
XX The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse
CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
CC cDNA sequence.
XX
XX Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;
Query Match 100.0%; Score 198; DB 24; Length 2100;
Best Local Similarity 100.0%; Pred. No. 1.3e-58;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTACTAGTTAAACAGGAGCGCTT 60
DB 916 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTACTAGTTAAACAGGAGCGCTT 975
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTCCACTGTGA 120
DB 976 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTCCACTGTGA 1035
QY 121 GGAGGGCTCACGGATTGGAGCCCAAGTGAAGCCCTTGGACCGACGATCTTAAGTGCTAC 180
DB 1036 GGAGGGCTCACGGATTGGAGCCCAAGTGAAGCCCTTGGACCGACGATCTTAAGTGCTAC 1095
QY 181 CCAGGGTGCAAAATACCTA 198
DB 1096 CCAGGGTGCAAAATACCTA 1113
RESULT 3
AAV55041
ID AAV55041 standard; cDNA; 2691 BP.
XX
XX AAV55041;
XX
XX 13-NOV-1998 (first entry)
XX
XX Murine XIAP coding sequence.
XX
XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein; ss.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FH

AC AAZ48862;
 XX 24-MAR-2000 (first entry)
 DT Human XIAP coding sequence.
 XX
 DE Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
 XX transforming growth factor-beta activated kinase 1; monocyte migration;
 KW TAK1 binding protein 1; extracellular matrix protein production;
 KW cell growth inhibitor; beta-amyloid protein deposition;
 KW immunosuppression; Transforming growth factor-beta; ds.
 XX
 OS Homo sapiens.
 XX
 XX JP11326328-A.
 PN 26-NOV-1999.
 XX
 PD 13-MAY-1998; 98JP-0130378.
 XX
 PF 13-MAY-1998; 98JP-0130378.
 XX
 PR 13-MAY-1998; 98JP-0130378.
 XX
 PA (MATS/) MATSUMOTO K.
 XX
 XX WPI; 2000-078337/07.
 DR P-PSDB; AAY59451.
 XX
 XX Screening a substance which inhibits combination of the X-linked
 PT inhibitor of apoptosis protein -
 XX
 PS Disclosure; Page 28-30; 43pp; Japanese.
 XX
 CC This sequence encodes the human XIAP protein.
 CC The invention relates to a method for screening a substance inhibiting
 CC the formation of a complex between XIAP and TAB1, in which X-linked
 CC inhibitor of apoptosis protein (XIAP), transforming growth factor-beta
 CC activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be
 CC tested are contacted with each other and then the presence or formation
 CC of a complex between XIAP and TAB1 is detected. The substance or formation
 CC as a drug for extracellular matrix protein production enhancement, cell
 CC growth inhibition, monocyte migration, physiologically active substance
 CC induction, immunosuppression, and beta-amyloid protein deposition. A
 CC substance inhibiting the formation of a complex between TAB1 and XIAP as
 CC well as between XIAP and TGF-beta (Transforming growth factor-beta) type
 CC I and/or type II receptor is useful as a drug.
 XX
 SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;

Query Match 87.4%; Score 173; DB 21; Length 1659;
 Best Local Similarity 92.4%; Pred. No. 6.3e-50;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGGATATACATCAAGTAAAGGAGCAGCTT 60
 DB 874 TATGAGCAGCGATCGTTACTTTTGGACATGGATATACATCAAGTAAAGGAGCAGCTT 933
 QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAGCGGATGAAGTGAAGTGTTCACCTGTGA 120
 DB 934 GCAAGAGCTGGATTTTATGCTTTAGGTGAGCGGATGAAGTGAAGTGTTCACCTGTGA 993
 QY 121 GGAGGCTCACGATTTGAAGCAAGTGAAGCCCTGGGACCGATGCTTAAGTGTCTAC 180
 DB 994 GGAGGCTAACGTATTGGAAGCCAGTGAAGCCCTGGGACCGATGCTTAAGTGTCTAC 1053
 QY 181 CCAGGCTGCAATACCT 197
 DB 1054 CCAGGCTGCAATATCT 1070

RESULT 6
 ID AAK99405
 XX AAK99405 standard; DNA; 2404 BP.

AC AAK99405;
 XX 27-JUN-2002 (first entry)
 DT DNA of APP related human homologue hCP35211.
 DE
 XX Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;
 KW amyloid precursor protein; tissue-specific expression control; human APP;
 KW APP pathway modulator; gene therapy; gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 692..1528
 FT /*tag- a
 FT /product= "Protein of human homologue hCP35211"
 FT /note= "No start codon"
 PN WC020226820-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 01-OCT-2001; 2001WO-EP11345.
 XX
 PR 29-SEP-2000; 2000US-236893P.
 PR 14-JUN-2001; 2001US-298309P.
 XX
 PA (NOVS) NOVARTIS AG
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX
 PI Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
 PI Reinhardt MWM, Zusman S;
 XX WPI; 2002-315796/35.
 P-PSDB; RAO20511.
 XX
 XX New transgenic fly, containing DNA encoding an Abeta portion of human
 XX APP, useful for identifying agents which modulate the APP pathway and
 XX which can be used to treat Alzheimer's disease -
 XX
 XX Example 4; Page 111; 129pp; English.

The invention relates to a transgenic fly whose genome comprises DNA
 encoding a polypeptide having the Abeta portion of human amyloid
 precursor protein (APP), fused to a signal sequence. The DNA sequence
 encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
 the specification. The DNA sequence is operably linked to a tissue-
 specific expression control sequence. Expression of the sequence gives
 the fly an altered phenotype. The purpose of the invention is for
 identifying agents that inhibit or promote the expression and/or function
 of genes or encoded polypeptides which modify the APP pathway. The agent
 is a compound, triple helix DNA, antisense oligonucleotide, double
 stranded RNA molecule, ribozyme, or particularly an antibody. It is used
 to treat conditions such as Alzheimer's disease. The agent can be used as
 an APP pathway modulator or in gene therapy. This polynucleotide sequence
 represents the DNA of the APP related human homologue hCP35211.
 SQ Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 other;

Query Match 87.4%; Score 173; DB 24; Length 2404;
 Best Local Similarity 92.4%; Pred. No. 7.3e-50;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGGATATCAAGTAAAGGAGCAGCTT 60
 DB 827 TATGAGCAGCGATCGTTACTTTTGGACATGGATATCAAGTAAAGGAGCAGCTT 886
 QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAGCGGATGAAGTGAAGTGTTCACCTGTGA 120
 DB 887 GCAAGAGCTGGATTTTATGCTTTAGGTGAGCGGATGAAGTGAAGTGTTCACCTGTGA 946
 QY 121 GGAGGCTCACGATTTGAAGCAAGTGAAGCCCTGGGACCGATGCTTAAGTGTCTAC 180

Db 947 GGAGGGCTAACTGATTGGAGAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1006

QY 181 CCAGGGTGCACAAATACCT 197
 Db 1007 CCAGGGTGCACAAATATCT 1023

RESULT 7
 AAT70836

ID AAT70836 standard; cDNA; 2540 BP.

AC AAT70836;

XX 02-SEP-1997 (first entry)

XX Human apoptosis inhibitor xiap cDNA.

XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;
 KW XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;
 KW ischaemia; myocardial infarction; stroke;
 KW reperfusion injury; toxin-induced liver disease; gene therapy;
 KW diagnosis; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 34..1527
 FT /*tag= a

XX W09706255-A2.

XX 20-FEB-1997.

XX 05-AUG-1996; 96WO-IB01022.

XX 22-DEC-1995; 95US-0576956.

XX 04-AUG-1995; 95US-0511485.

XX (UYOT-) UNIV OTTAWA.

XX Balrd S, Korneluk RG, Liston P, Mackenzie AE;

XX WPI; 1997-154262/14.
 DR P-PSDB; AAW19581.

XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
 PT of susceptibility to apoptotic disease

XX Claim 12; Page 67-68; 219pp; English.

XX Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and
 CC hiap-2 genes (AAT70836-41) respectively code for a new class of
 CC mammalian proteins (AAW19581-86) that are inhibitors of apoptosis
 CC (IAP). The xiap gene (for X-linked IAP gene) was isolated from a
 CC human foetal brain zapII cDNA library using an X-linked sequence
 CC tag site that shows strong homology with the conserved ring zinc
 CC finger domain of baculovirus CpiAP and OpiAP genes. The gene was
 CC assigned to chromosome Xq25 by FISH. IAP nucleic acids can be used
 CC to express IAP polypeptides in cells and animals to inhibit
 CC apoptosis, and as primers and probes to identify and isolate
 CC additional IAP genes, as well as in methods for treating diseases
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).

XX Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 1 other;

Query Match 87.4%; Score 173; DB 18; Length 2540;

Best Local Similarity 92.4%; Pred. No. 7.5e-50;

Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCATCTTACTTTTGGACATCGATATCTCAGTTAAACAGGACGCTT 60

Db 826 TATGAAGCAGCATCTTACTTTTGGACATCGATATCTCAGTTAAACAGGACGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGATAAAGTCTTCCACTGTGGA 120
 Db 886 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGATAAAGTCTTCCACTGTGGA 945
 QY 121 GGAGGGCTCAGGGATTGGAAGCCCAAGTGAAGCCCTTGGACCAGCATGCTAAATGCTAC 180
 Db 946 GGAGGGCTCAGGGATTGGAAGCCCAAGTGAAGCCCTTGGACCAGCATGCTAAATGCTAC 180
 QY 181 CCAGGGTGCACAAATACCT 197
 Db 1006 CCAGGGTGCACAAATATCT 1022

RESULT 8

AAA64901
 ID AAA64901 standard; DNA; 2540 BP.

XX AAA64901;

XX 07-NOV-2000 (first entry)

XX Human X-linked inhibitor of apoptosis DNA.

XX X-linked inhibitor of apoptosis; XIAP; hILP; MIHA; U45880;
 KW antisense; antiinflammatory; cytostatic; tumour; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 34..1527
 FT /*tag= a
 FT /product= "X-linked inhibitor of apoptosis"

XX US6087173-A.

XX 11-JUL-2000.

XX 09-SEP-1999; 99US-0392580.

XX 09-SEP-1999; 99US-0392580.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CP, Cowser LM, Ackermann EJ;

XX WPI; 2000-498201/44.
 DR P-PSDB; AAY99985.

XX Antisense compound useful for research reagents, diagnostics,
 PT prophylaxis and for treating disorders associated with X-linked
 PT inhibitor of apoptosis, modulates expression of X-linked inhibitor of
 PT apoptosis

XX Example 13; Column 43-48; 33pp; English.

XX The present invention relates to antisense oligonucleotides designed to
 CC inhibit expression of the human X-linked inhibitor of apoptosis. The
 CC present sequence is the X-linked inhibitor of apoptosis DNA.
 CC Modified phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are
 CC more effective inhibitors than unmodified oligonucleotides. The
 CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
 CC expression in cells and tissues in vitro. The oligonucleotides are also
 CC useful for treating animals or humans, prone to a disease associated
 CC with X-linked inhibitor of apoptosis. The oligonucleotides may also be
 CC used prophylactically to prevent infection, inflammation or tumour
 CC formation.

XX Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 other;

Query Match 87.4%; Score 173; DB 21; Length 2540

Best Local Similarity 92.4%; Pred. No. 7.5e-50;

Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

enhancing apoptosis in a cell, comprising administering a negative regulator of the IAP anti-apoptotic pathway to the cell. The IAP antisense inhibitor is useful for enhancing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for treating a patient diagnosed with a proliferative disease like cancer. The IAP antisense molecule is useful to treat, ameliorate, improve, sustain or prevent proliferative diseases (e.g. ovarian cancer, adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or conditions where apoptosis is involved or implicated (e.g. embryonic development, viral pathogenesis, autoimmune disorders, neurodegenerative diseases, multiple sclerosis, lupus erythematosus and infection by herpes virus, pox virus and adenovirus). The present sequence is a human IAP cDNA sequence.

XX Sequence 3000 BP; 974 A; 452 C; 601 G; 973 T; 0 other;

Query Match 87.4%; Score 173; DB 24; Length 3000;

Best Local Similarity 92.4%; Pred. No. 8e-50;

Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTACTTTGGACATGGATATCTACAGTAAAGGACGACTT 60

DB 1482 TATGAAGCAGCGATCTTACTTTGGACATGGATATCTACAGTAAAGGACGACTT 1541

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTCTCCACTGTGGA 120

DB 1542 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTCTCCACTGTGGA 1601

QY 121 GGAGGGCTCAGGATTTGGAGCCCAAGTGAAGACCCCTGGGACCAAGTCTTAAGTGTCTAC 180

DB 1602 GGAGGGCTCAGGATTTGGAGCCCAAGTGAAGACCCCTGGGACCAAGTCTTAAGTGTCTAC 1661

QY 181 CCAGGGTGCAAAATACCT 197

DB 1662 CCAGGGTGCAAAATACCT 1678

RESULT 11

AAV55038

ID AAV55038 standard; cDNA; 5232 BP.

XX AAV55038;

AC AAV55038;

DT 13-NOV-1998 (first entry)

XX Human XIAP coding sequence.

XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;

XX proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 34..1527

XX /tag= a

XX /product= XIAP

XX WO9835693-A2.

XX 20-AUG-1998.

XX 13-FEB-1998; 98WO-IB00781.

XX 13-FEB-1997; 97US-0800929.

XX (UYOT-) UNIV OTTAWA.

XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;

XX Tsang B;

XX WPI: 1998-467164/40.

XX P-PSDB; AAW69294.

XX

PT Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP or NAIP polypeptide - also methods for prognosis based on presence of IAP and NAIP, specifically applied to cancers involving p53 mutations

XX Claim 13: Fig 1; 147pp; English.

XX This sequence encodes the human XIAP protein, which is an inhibitor of apoptosis protein (IAP), and can be used in the method of the invention.

CC The method is for enhancing apoptosis in cells from a mammal with proliferative disease by treatment with a compound that inhibits biological activity of an IAP or NAIP polypeptide. The inhibitory compounds are used to treat proliferative diseases, specifically cancers of ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,

CC liver nasopharynx, thyroid, central nervous system, prostate, colon, rectum, cervix or endometrium, particularly to increase their sensitivity to chemotherapeutic agents. High levels of the IAP or NAIP proteins are detected in many cancers and are associated with poor prognosis,

CC resistance to chemotherapeutic agents and mutations in p53 (it is suggested that wild-type p53 suppresses transcription of the IAP or NAIP genes). Transgenic animals are used for testing the effects of antisense oligonucleotides and for screening for the inhibitors.

CC

XX Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;

QY Query Match 87.4%; Score 173; DB 19; Length 5232;

Best Local Similarity 92.4%; Pred. No. 1e-49;

Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTACTTTGGACATGGATATCTACAGTAAAGGACGACTT 60

DB 826 TATGAAGCAGCGATCTTACTTTGGACATGGATATCTACAGTAAAGGACGACTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTCTCCACTGTGGA 120

DB 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTCTCCACTGTGGA 945

QY 121 GGAGGGCTCAGGATTTGGAGCCCAAGTGAAGACCCCTGGGACCAAGTCTTAAGTGTCTAC 180

DB 946 GGAGGGCTCAGGATTTGGAGCCCAAGTGAAGACCCCTGGGACCAAGTCTTAAGTGTCTAC 1005

QY 181 CCAGGGTGCAAAATACCT 197

DB 1006 CCAGGGTGCAAAATACCT 1022

RESULT 12

AA03575

ID AA03575 standard; cDNA; 1752 BP.

XX AA03575;

XX 19-JUN-2001 (first entry)

XX Human IAP-like protein-3 (ILP-3) cDNA.

XX Human; inhibitor of apoptosis; IAP-like protein-3; ILP-3;

XX chromosome 2q12-q14; transforming growth factor beta receptor; TGFbetaR;

XX c-Jun N-terminal kinase; JNK; gene therapy; osteoarthritis; cytostatic;

XX hypothyroidism; juvenile nephronophthisis; thrombophilia; cancer;

XX colorectal cancer; neonatal purpura fulminans; autoimmune disease;

XX diabetes; multiple sclerosis; neurodegenerative disease;

XX retinal degeneration; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 847..1197

XX /tag= a

XX /product= "Human inhibitor of apoptosis (IAP)-like protein-3 (hILP-3)"

XX WO200123568-A2.

XX

XX 05-APR-2001.
XX 29-SEP-2000; 2000WO-US26735.
XX 30-SEP-1999; 99US-0157169.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Duckett C, Mir SS;
XX WPI; 2001-258135/26.
XX P-PSDB; AAE00359.
XX Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
XX transforming growth factor beta receptor modulating activity, and the
XX nucleic acids that encode them, useful for treating, e.g. diabetes and
XX multiple sclerosis .
XX Claim 18; Page 87-88; 108pp; English.
XX The present sequence is human inhibitor of apoptosis (IAP)-like protein-3
XX (ILP-3) cDNA. The hILP-3 gene is located on chromosome 2q12-q14.
XX ILP-3 comprises a spacer region and a ring finger domain. The ILP
XX interacts with transforming growth factor beta receptor (TGFbetaR) and
XX modulates TGFbetaR activity. ILP-3 also moderately inhibits ILP-1
XX mediated c-Jun N-terminal kinase (JNK) activation when co-transfected
XX with ILP-1. Such activity decreases or prevents apoptosis in a cell.
XX ILP-3 is used in the area of genetic testing for predisposition to
XX diseases, such as osteoarthritis, hypothyroidism, juvenile
XX nephronophthisis, thrombophilia, colorectal cancer and neonatal purpura
XX fulminans owing to an ILP-3 deletion or mutation. The ILP is also used
XX in the treatment of diseases associated with abnormal apoptosis such as
XX cancer, autoimmune diseases, e.g., diabetes and multiple sclerosis and
XX neurodegenerative diseases including retinal degeneration. The ILP-3
XX gene is also used in gene therapy for treating patients suffering from
XX ILP-3 gene deletions or mutations.
XX Sequence 1752 BP; 530 A; 299 C; 385 G; 538 T; 0 other;

Query Match 79.3%; Score 157; DB 22; Length 1752;
Best Local Similarity 87.3%; Pred. No. 2.4e-44;
Matches 172; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATGTTTACTTTGGACATGATATCTACTAGTTAAACAGGAGCAGCTT 60
DB 499 TATGAAGCATGGATCATTTACTTTGGGATGCGATATATTCAGTTAAACAGGAGCAGCTT 558
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGGA 120
DB 559 TCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGGA 618
QY 121 GGAGGGCTCAGGATTTGAAGCCAGTGAAGCCCTGGGACCAGCAGCTGAAGTCTTAC 180
DB 619 GGGGGGCTAACTGATTTGAAGCCAGCAGCAGCCTTGGGAACAACATGATAAATGGCAT 678
QY 181 CCAGGGTGCATAATACCT 197
DB 679 CCAGGGTGTAAATATCT 695

RESULT 13
ABK14677
ID ABK14677 standard; cDNA; 1758 BP.
XX AC ABK14677;
XX 08-MAY-2002 (first entry)
XX Human Inhibitor of apoptosis protein 7 (IAPL7) cDNA.
XX Human; gene; inhibitor of apoptosis 7; IAPL7; cytostatic;
KW antiapoptotic; IAP; apoptosis; antibody; V-Rel; NF-kappaB;

KW chromosome 19; vaccine; gene therapy; hyperproliferative disease;
KW cancer; transgenic animal; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 286..1680
XX FT /*tag= a
XX FT /product= "IAPL7 protein"
XX FT /partial
XX FT /note= "No start codon shown"
XX W0200210381-A1.
XX 07-FEB-2002.
XX 18-JUL-2001; 2001WO-EP08287.
XX 28-JUL-2000; 2000EP-0116452.
XX (MERE) MERCK PATENT GMBH.
XX Hentsch B;
XX WPI; 2002-188741/24.
XX P-PSDB; AAU75747.
XX New inhibitor of apoptosis proteins and polynucleotides useful in
XX vaccines for inducing an immune response against hyperproliferative
XX diseases e.g. cancer
XX Claim 5; Page 33-35; 41pp; English.
XX This invention relates to the nucleic acid and protein sequences of a
XX novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences
XX have homology to the IAP (inhibitors of apoptosis) gene family which
XX are thought to inhibit proteins by regulating the anti-apoptotic
XX activity of the V-Rel and NF-kappaB family of transcription factors.
XX The gene for IAPL7 is located on human chromosome 19. The nucleic acids
XX of the invention are useful for screening to identify compounds that
XX stimulate or inhibit the function or level of IAPL7, where the
XX identified compounds are useful for treating hyper-proliferative
XX diseases such as cancer. The protein sequences may also be used to
XX identify membrane bound or soluble receptors of IAPL7 by standard
XX receptor binding techniques. Nucleic acids encoding IAPL7 may be used
XX as hybridisation probes for cDNA and genomic DNA, or as primers for
XX nucleic acid amplification reaction and the primers and probes may also
XX be used to isolate full-length cDNAs and genomic clones encoding IAPL7.
XX The nucleic acid sequences are useful as diagnostic reagents for
XX diagnosing a disease or a susceptibility to a disease by detecting
XX mutations in the associated gene. The nucleic acid sequence is useful
XX for chromosome localisation and tissue expression studies and is also
XX useful for producing transgenic animals. The IAPL7 protein sequence may
XX also be used to generate an anti-IAPL7 antibody which is useful in
XX screening methods for detecting the effect of added compounds on the
XX production of mRNA and protein in cells. The sequences of the invention
XX are also useful as vaccines for inducing an immunological response in a
XX mammal. The present sequence represents the cDNA encoding the human
XX inhibitor of apoptosis 7 (IAP7) protein of the invention.
XX Sequence 1758 BP; 488 A; 371 C; 470 G; 429 T; 0 other;

Query Match 75.3%; Score 149; DB 24; Length 1758;
Best Local Similarity 84.8%; Pred. No. 1.5e-41;
Matches 167; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATGTTTACTTTGGACATGATATCTACTAGTTAAACAGGAGCAGCTT 60
DB 979 TATGAAGCCCGGCTCATTTACTTTGGACATGATGATCTCCGTTAAACAGGAGCAGCTT 1038
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGGA 120
DB 1039 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGGA 1098

DR P-PSDB; AAE00365.

XX

PT Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with

PT transforming growth factor beta receptor modulating activity, and the

PT nucleic acids that encode them, useful for treating, e.g. diabetes and

XX multiple sclerosis -

XX

PS Claim 18; Page 94-98; 108pp; English.

PS

XX

CC The present sequence is human inhibitor of apoptosis (IAP)-like protein-2

CC (ILP-2) cDNA. The hILP-2 gene is located on chromosome 19q13.3-q13.4

CC ILP-2 comprises a single amino-terminal domain known as baculovirus iap

CC repeat (BIR), followed by a spacer region and a carboxy-terminal ring

CC finger domain. It interacts with transforming growth factor beta

CC receptor (TGFbetaR) and modulates TGFbetaR activity. It also potentially

CC inhibits apoptosis induced by overexpression of Bax or by Caspase-9 and

CC Apaf-1. It also activates c-Jun N-terminal kinase (JNK) activity. ILP-2

CC is used in the area of genetic testing for predisposition to diseases,

CC such as cone-rod retinal dystrophy-2, retinitis pigmentosa,

CC glutaricaciduria, T-cell acute lymphoblastic leukaemia, colorectal cancer

CC and hyperferritinemia-cataract syndrome owing to an ILP-2 deletion or

CC mutation. The ILP is also used in the treatment of diseases associated

CC with abnormal apoptosis such as cancer, autoimmune diseases, e.g.,

CC diabetes and multiple sclerosis and neurodegenerative diseases including

CC retinal degeneration. The ILP-2 gene is also used in gene therapy for

CC treating patients suffering from ILP-2 gene deletions or mutations.

XX

XX

Sequence 4993 BP; 1526 A; 973 C; 1196 G; 1297 T; 1 other;

XX

Query Match	75.3%	Score 149;	DB 22;	Length 4993;
Best Local Similarity	84.88;	Pred. No. 2.3e-41;		
Matches 167;	Conservative 0;	Mismatches 30;	Indels 0;	Gaps 0;
OY 1	TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGACGAGCTT	60		
Db				
2083	TATGAAGCCGGCTCATCTACTTTTGGACATGGATGCTACTCCGTTTAAACAAGACGAGCTT	2142		
OY 61	GCAAGAGCTGGATTTTATGCTTTTAGTGTGAAGCGGATAAAGTGAATGCTTCCACTGTGGA	120		
Db				
2143	GCAAGAGCTGGATTTTATGCTTATAGTTCAGAGGATTAAGTACATGCTTTCACCTGTGGA	2202		
OY 121	GGAGGGCTCACGGATTGGAGCCAAAGTGAAGACCCCTGGGACCATGCTAAAGTGTAC	180		
Db				
2203	GGAGGGCTTAGCCAACTGGAGCCCAAGGAAGATCTTGGGAACAGCATGCTAAATGGTAT	2262		
OY 181	CCAGGGTGCAAATACCT	197		
Db				
2263	CCAGGTGCGAAATATCT	2279		
Db				

Search completed: April 19, 2003, 01:52:57
Job time : 157 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2003, 01:53:06 ; Search time 43 Seconds
(without alignments)
1412.140 Million cell updates/sec

Title: US-09-654-743-51

Perfect score: 198

Sequence: 1 tatgaagcagcgatgttac.....accaggggtgcaataccta 198

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_NA.*
1: /cgn2_6/ptodata/1/lna/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/lna/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/lna/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/lna/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/lna/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/lna/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	100.0	2100	2	US-08-511-485-9
2	194.8	98.4	2691	3	US-09-212-971-9
3	194.8	98.4	2691	3	US-08-800-929A-9
4	194.8	98.4	2691	4	US-09-617-053A-9
5	173	87.4	1588	4	US-09-239-867-3
6	173	87.4	2540	2	US-08-511-485-3
7	173	87.4	2540	3	US-09-332-580-1
8	173	87.4	5232	3	US-09-212-971-3
9	173	87.4	5232	3	US-08-800-929A-3
10	173	87.4	711	3	US-09-121-979-3
11	147.4	74.4	711	3	US-09-332-319-3
12	147.4	74.4	1559	4	US-09-239-867-1
13	147.4	74.4	15231	3	US-08-128-155-16
14	134.4	67.9	15231	3	US-09-121-979-3
15	109.6	55.4	176373	3	US-09-128-155-17
16	76	38.4	2601	4	US-08-569-749-3
17	76	38.4	2601	5	PCT-US96-12860-3
18	76	38.4	2676	2	US-08-511-485-5
19	76	38.4	3076	2	US-09-205-144-1
20	76	38.4	6669	3	US-09-212-971-5
21	76	38.4	6669	3	US-08-800-929A-5
22	76	38.4	6669	4	US-09-617-053A-5
23	68	34.3	2676	3	US-09-212-971-11
24	68	34.3	2676	3	US-08-800-929A-11
25	68	34.3	2676	4	US-09-617-053A-11
26	65.8	33.2	1435	5	PCT-US95-05922A-1
27	65.8	33.2	2580	2	US-08-511-485-7

28 65.8 33.2 2589 4 US-08-569-749-1 Sequence 1, Appli
29 65.8 33.2 2589 5 PCT-US96-12860-1 Sequence 1, Appli
30 65.8 33.2 3532 2 US-09-205-204-1 Sequence 1, Appli
31 65.8 33.2 3532 3 US-09-212-971-7 Sequence 7, Appli
32 65.8 33.2 3732 3 US-08-800-929A-7 Sequence 7, Appli
33 65.8 33.2 3732 4 US-09-617-053A-7 Sequence 7, Appli
34 61 30.8 2862 4 US-08-569-749-13 Sequence 13, Appli
35 61 30.8 2862 5 PCT-US96-12860-13 Sequence 13, Appli
36 61 30.8 3151 3 US-09-212-971-13 Sequence 13, Appli
37 61 30.8 3151 3 US-08-800-929A-13 Sequence 13, Appli
38 61 30.8 3151 4 US-09-617-053A-13 Sequence 13, Appli
39 45 22.7 5502 3 US-08-836-134-1 Sequence 1, Appli
40 45 22.7 5502 4 US-09-493-784-1 Sequence 1, Appli
41 27.6 13.9 2160 4 US-09-372-668-1 Sequence 1, Appli
42 27.6 13.9 98844 4 US-09-791-211-10 Sequence 10, Appli
43 26.8 13.5 426 4 US-09-283-144-2 Sequence 2, Appli
44 26.8 13.5 1165 3 US-08-448-722A-1 Sequence 1, Appli
45 26.8 13.5 1165 4 US-08-189-309B-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-511-485-9
; Sequence 9, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-9

Query Match 100.0%; Score 198; DB 2; Length 2100;
Best Local Similarity 100.0%; Pred. No. 1-2e-61;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TATGAAGCAGCGATGTTCCTTTGGACATGGATACACTAGTAAAGGACAGCTT 60
|||||

Db 916 TATGAAGCACGGATCGTTACTTTTGGAACTGGATATACGTACAGTTAAACAGGACGACGTT 975
QY 61 CCAAGAGCTGGATTTATGCTTTTAGGTGAAGCCGATTAAGTGAAGTCTTCCACTGTGGA 120
Db 976 CCAAGAGCTGGATTTATGCTTTTAGGTGAAGCCGATTAAGTGAAGTCTTCCACTGTGGA 1035
QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 180
Db 1036 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 1095
QY 181 CCAGGGTGCAAAATACCTA 198
Db 1096 CCAAGGGTGCAAAATACCTA 1113

RESULT 2

US-09-212-971-9
; Sequence 9, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; EARLIER FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-212-971-9

Query Match 98.4%; Score 194.8; DB 3; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1.9e-60;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCGTTACTTTTGGAACTGGATATACGTACAGTTAAACAGGACGACGTT 1520
Db 1461 TATGAAGCACGGATCGTTACTTTTGGAACTGGATATACGTACAGTTAAACAGGACGACGTT 1520
QY 61 CCAAGAGCTGGATTTATGCTTTTAGGTGAAGCCGATTAAGTGAAGTCTTCCACTGTGGA 120
Db 1521 CCAAGAGCTGGATTTATGCTTTTAGGTGAAGCCGATTAAGTGAAGTCTTCCACTGTGGA 1580
QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 180
Db 1581 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 1640
QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAAGGGTGCAAAATACCTA 1658

RESULT 3

US-08-800-929A-9
; Sequence 9, Application US/08800929A
; Patent No. 613437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G

APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-800-929A-9

Query Match 98.4%; Score 194.8; DB 3; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1.9e-60;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCGTTACTTTTGGAACTGGATATACGTACAGTTAAACAGGACGACGTT 60
Db 1461 TATGAAGCACGGATCGTTACTTTTGGAACTGGATATACGTACAGTTAAACAGGACGACGTT 1520
QY 61 CCAAGAGCTGGATTTATGCTTTTAGGTGAAGCCGATTAAGTGAAGTCTTCCACTGTGGA 120
Db 1521 CCAAGAGCTGGATTTATGCTTTTAGGTGAAGCCGATTAAGTGAAGTCTTCCACTGTGGA 1580
QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 180
Db 1581 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 1640
QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAAGGGTGCAAAATACCTA 1658

RESULT 4

US-09-617-053A-9
; Sequence 9, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:

```

; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-617-053A-9

Query Match      98.4%; Score 194.8; DB 4; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1.9e-60;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGAGCAGCTT 60
DB 1461 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGAGCAGCTT 1520

QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAGTGAAGTGCCTCCACTGTGGA 120
DB 1521 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAGTGAAGTGCCTCCACTGTGGA 1580

QY 121 GGAGGCTCAGCGATTGGAAGCGGATGAAGACCCCTGGGACCGATGCTTAAGTGTCTAC 180
DB 1581 GGAGGCTCAGCGATTGGAAGCGGATGAAGACCCCTGGGACCGATGCTTAAGTGTCTAC 1640

QY 181 CCAGGGTCAAAATACCTA 198
DB 1641 CCAGGGTCAAAATACCTA 1658

RESULT 5
US-09-239-867-3
; Sequence 3, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-239-867-3

Query Match      87.4%; Score 173; DB 4; Length 1588;
Best Local Similarity 92.4%; Pred. No. 1.1e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGAGCAGCTT 60
DB 826 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAGTGAAGTGCCTCCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAGTGAAGTGCCTCCACTGTGGA 945

QY 121 GGAGGCTCAGCGATTGGAAGCGGATGAAGACCCCTGGGACCGATGCTTAAGTGTCTAC 180
DB 946 GGAGGCTCAGCGATTGGAAGCGGATGAAGACCCCTGGGACCGATGCTTAAGTGTCTAC 1005

QY 181 CCAGGGTCAAAATACCT 197

; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-3

Query Match      87.4%; Score 173; DB 2; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.3e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGAGCAGCTT 60
DB 826 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAGTGAAGTGCCTCCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAGTGAAGTGCCTCCACTGTGGA 945

QY 121 GGAGGCTCAGCGATTGGAAGCGGATGAAGACCCCTGGGACCGATGCTTAAGTGTCTAC 180
DB 946 GGAGGCTCAGCGATTGGAAGCGGATGAAGACCCCTGGGACCGATGCTTAAGTGTCTAC 1005

QY 181 CCAGGGTCAAAATACCT 197
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Db 1006 CCAGGGTGCAAAATATCT 1022
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RESULT 7

US-09-392-580-1
; Sequence 1, Application US/09392580
; Patent No. 6087173
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION
; FILE REFERENCE: RTS-0072
; CURRENT APPLICATION NUMBER: US/09/392,580
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(1527)
US-09-392-580-1

Query Match 87.4%; Score 173; DB 3; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.3e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATGCTTACTTTTGGACATGGATATATCTCAGTTAAACAGGAGCAGCTT 60
|||||
Db 826 TATGAAGCAGCGATGCTTACTTTTGGACATGGATATATCTCAGTTAAACAGGAGCAGCTT 885
|||||
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGATTAAGTGAAGTGCCTTCCACTGTGGA 120
|||||
Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGATTAAGTGAAGTGCCTTCCACTGTGGA 945
|||||
QY 121 GGAGGGCTCAGGATTTGGAAGCCAAAGTGAAGACCCCTGGGACCATGCTTAAGTGTCTAC 180
|||||
Db 946 GGAGGGCTTAAGTGAAGCCCAAGTGAAGACCCCTGGGACCATGCTTAAGTGTCTAC 1005
|||||
QY 181 CCAGGGTGCAAAATACCT 197
|||||
Db 1006 CCAGGGTGCAAAATATCT 1022

RESULT 8

US-09-212-971-3
; Sequence 3, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030,590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

LENGTH: 5232
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (4623)...(4623)
OTHER INFORMATION: n can be any nucleotide
FEATURE:
NAME/KEY: variation
LOCATION: (4622)...(4622)
OTHER INFORMATION: n can be any nucleotide
US-09-212-971-3

Query Match 87.4%; Score 173; DB 3; Length 5232;
Best Local Similarity 92.4%; Pred. No. 1.9e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATGCTTACTTTTGGACATGGATATATCTCAGTTAAACAGGAGCAGCTT 60
|||||
Db 826 TATGAAGCAGCGATGCTTACTTTTGGACATGGATATATCTCAGTTAAACAGGAGCAGCTT 885
|||||
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGATTAAGTGAAGTGCCTTCCACTGTGGA 120
|||||
Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGATTAAGTGAAGTGCCTTCCACTGTGGA 945
|||||
QY 121 GGAGGGCTCAGGATTTGGAAGCCAAAGTGAAGACCCCTGGGACCATGCTTAAGTGTCTAC 180
|||||
Db 946 GGAGGGCTTAAGTGAAGCCCAAGTGAAGACCCCTGGGACCATGCTTAAGTGTCTAC 1005
|||||
QY 181 CCAGGGTGCAAAATACCT 197
|||||
Db 1006 CCAGGGTGCAAAATATCT 1022

RESULT 9

US-08-800-929A-3
; Sequence 3, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER:

```
/ REFERENCE/DOCKET NUMBER: 07891/009001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-428-0200
/ TELEFAX: 617-428-7045
/
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5232 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: Other
/ LOCATION: 1..5232
/ OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.
US-08-800-929A-3

Query Match      87.4%; Score 173; DB 3; Length 5232;
Best Local Similarity 92.4%; Pred. No. 1.9e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 60
DB 826 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAGTGAAGTGCCTTCCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAGTGAAGTGCCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGCGATTGGAAGCAAGTGAAGACCCCTGGGACCCAGCAGCTTAAGTGCTAC 180
DB 946 GGAGGGCTCAGCGATTGGAAGCAAGTGAAGACCCCTGGGACCCAGCAGCTTAAGTGCTAC 180
QY 181 CCAGGGTGCAAAATACCT 197
DB 1006 CCAGGGTGCAAAATATCT 1022

RESULT 11
US-09-121-979-3
; Sequence 3, Application US/09121979
; Patent No. 6159709
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021001
; CURRENT APPLICATION NUMBER: US/09/121.979
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-121-979-3

Query Match      74.4%; Score 147.4; DB 3; Length 711;
Best Local Similarity 84.3%; Pred. No. 1.2e-43;
Matches 166; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 60
DB 10 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 69
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAGTGAAGTGCCTTCCACTGTGGA 120
DB 70 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAGTGAAGTGCCTTCCACTGTGGA 129
QY 121 GGAGGGCTCAGCGATTGGAAGCAAGTGAAGACCCCTGGGACCCAGCAGCTTAAGTGCTAC 180
DB 130 GGAGGGCTCAGCGATTGGAAGCAAGTGAAGACCCCTGGGACCCAGCAGCTTAAGTGCTAC 180
QY 181 CCAGGGTGCAAAATACCT 197
DB 190 CCAGGGTGCAAAATATCT 206

RESULT 12
US-09-332-319-3
; Sequence 3, Application US/09332319
; Patent No. 6171821
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021002
; CURRENT APPLICATION NUMBER: US/09/332.319
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; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: 09/121,979
; EARLIER FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-332-319-3

Query Match 74.4%; Score 147.4; DB 4; Length 711;
Best Local Similarity 84.3%; Pred. No. 1.2e-43;
Matches 166; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGGATCTTACTTTGGACATGGATATACCTAGTTAACAGGAGCAGCTT 60
DB 10 TATGAAGCAGCGGATCTTACTTTGGACATGGATATACCTAGTTAACAGGAGCAGCTT 69
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 120
DB 70 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 129
QY 121 GGAGGCTCAGCGATTTGGAAGCAAGTGAAGCCCTGGACCATGCTTAAGTGTCTAC 180
DB 130 GGAGGCTCAGCGATTTGGAAGCAAGTGAAGCCCTGGACCATGCTTAAGTGTCTAC 189
QY 181 CCAGGTGCAAAATACCT 197
DB 190 CCAGGTGCAAAATATCT 206

RESULT 13
US-09-239-867-1
; Sequence 1, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1559
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)-(1559)
; OTHER INFORMATION: n = A,T,C or G
US-09-239-867-1

Query Match 74.4%; Score 147.4; DB 4; Length 1559;
Best Local Similarity 84.3%; Pred. No. 1.8e-43;
Matches 166; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGGATCTTACTTTGGACATGGATATACCTAGTTAACAGGAGCAGCTT 60
DB 800 TATGAAGCAGCGGATCTTACTTTGGACATGGATATACCTAGTTAACAGGAGCAGCTT 859
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 120
DB 860 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 919
QY 121 GGAGGCTCAGCGATTTGGAAGCAAGTGAAGCCCTGGACCATGCTTAAGTGTCTAC 180
DB 920 GGAGGCTCAGCGATTTGGAAGCAAGTGAAGCCCTGGACCATGCTTAAGTGTCTAC 979

QY 181 CCAGGTGCAAAATACCT 197
DB 980 CCAGGTGCAAAATATCT 996
RESULT 14
US-09-128-155-16/C
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)-(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Query Match 67.9%; Score 134.4; DB 3; Length 152331;
Best Local Similarity 83.2%; Pred. No. 7.1e-38;
Matches 164; Conservative 0; Mismatches 32; Indels 1; Gaps 1;
QY 1 TATGAAGCAGCGGATCTTACTTTGGACATGGATATACCTAGTTAACAGGAGCAGCTT 60
DB 3298 TATGAAGCAGCGGATCTTACTTTGGACATGGATATACCTAGTTAACAGGAGCAGCTT 3239
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 120
DB 3238 TCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGA 3179
QY 121 GGAGGCTCAGCGATTTGGAAGCAAGTGAAGCCCTGGACCATGCTTAAGTGTCTAC 180
DB 3178 GGGGGCTAAGTGTGGAGCCACCAGAA-AACCTTGGGACACATATAAATGGAT 3120
QY 181 CCAGGTGCAAAATACCT 197
DB 3119 CCAGGTGCAAAATATCT 3103

RESULT 15
US-09-128-155-17
; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2003, 02:27:21 ; Search time 66 Seconds
(without alignments)
3013.686 Million cell updates/sec

Title: US-09-654-743-51

Perfect score: 198

Sequence: 1 tatgaagcagcgtatcgttac.....accaggtgcaataaccta 198

Scoring table: IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

Searched: 639749 seqs, 502280978 residues

Total number of hits satisfying chosen parameters: 1279498

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	100.0	2100	9	US-09-201-936-9
2	194.8	98.4	2691	10	US-09-974-592-9
3	173	87.4	2404	9	US-09-964-899-38
4	173	87.4	2540	9	US-09-201-936-3
5	173	87.4	5232	10	US-09-974-592-3
6	134.4	67.9	152331	9	US-10-095-407-16
7	109.6	55.4	176373	9	US-10-095-407-17
8	76	38.4	2676	9	US-09-201-936-5
9	76	38.4	3076	9	US-09-954-531-16
10	76	38.4	3076	10	US-09-954-456-1635
11	76	38.4	6669	10	US-09-974-592-5
12	68	34.3	2450	9	US-09-201-936-39
13	68	34.3	2676	10	US-09-974-592-11
14	65.8	33.2	2580	9	US-09-201-936-7
15	65.8	33.2	3532	10	US-09-880-107-3354
16	65.8	33.2	3732	10	US-09-974-592-7
17	61	30.8	3151	10	US-09-974-592-13
18	59.4	30.0	2416	9	US-09-201-936-41
19	56.4	28.5	3773	9	US-10-041-859-1

Sequence 1, Appli
Sequence 21, Appli
Sequence 184, App
Sequence 2, Appli
Sequence 23, Appli
Sequence 21, Appli
Sequence 3493, Ap
Sequence 6697, Ap
Sequence 6, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 3000, Ap
Sequence 222, App
Sequence 1065, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 189, App
Sequence 3474, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 243, App
Sequence 274, App
Sequence 933, App
Sequence 2950, Ap

5504 8 US-08-913-322-1
6124 8 US-08-913-322-21
6124 10 US-09-967-768A-184
6133 8 US-08-913-322-2
6228 8 US-08-913-322-23
2291 10 US-09-778-927A-21
240 9 US-09-786-692-3493
240 9 US-09-786-692-6687
2326 9 US-10-011-585A-6
2790 10 US-09-739-254-30
2790 10 US-09-904-615-30
2000 9 US-09-938-842A-3000
1011 10 US-09-770-445-222
2265 9 US-09-938-842A-1065
1503841 9 US-09-946-807-1
1503841 10 US-09-795-668-1
1503841 10 US-09-795-668-1
3411 10 US-09-925-302-189
19172 10 US-09-764-877-3474
2160 9 US-10-115-195-1
6911 9 US-10-170-528-1
197997 10 US-09-822-246-3
75899 10 US-09-854-883-243
698 10 US-09-770-149-274
766 10 US-09-770-445-933
5031 10 US-09-764-877-2950

ALIGNMENTS

RESULT 1
US-09-201-936-9
; Sequence 9, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201.936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011.356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576.956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511.485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9

Query Match 100.0%; Score 198; DB 9; Length 2100;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTAGTTAAACAGGACAGCTT 60
|||||
Db 916 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTAGTTAAACAGGACAGCTT 975
Qy 61 GCAAGAGCTGGATTTATGCTTTTAGTGAAGCGGATAAGTGAAGTGTTCACGTGGA 120
|||||
Db 976 GCAAGAGCTGGATTTATGCTTTTAGTGAAGCGGATAAGTGAAGTGTTCACGTGGA 1035

QY 121 GGAGGGCTCAGGATTTGAAGCAAGTGAAGACCCCTGGGACCAAGCTGCTAAAGTGCTAC 180
|||||
Db 1036 GGAGGGCTCAGGATTTGAAGCAAGTGAAGACCCCTGGGACCAAGCTGCTAAAGTGCTAC 1095
QY 181 CCAGGGTGCAATACCTA 198
|||||
Db 1096 CCAGGGTGCAATACCTA 1113

RESULT 2
US-09-974-592-9
; Sequence 9, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-974-592-9

Query Match 98.4%; Score 194.8; DB 10; Length 2691;
Best Local Similarity 99.0%; Pred. No. 3.7e-58;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
|||||
Db 1461 TATGAAGCAGGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 1520
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGA 120
|||||
Db 1521 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGA 1580
QY 121 GGAGGGCTCAGGATTTGAAGCAAGTGAAGACCCCTGGGACCAAGCTGCTAAAGTGCTAC 180
|||||
Db 1581 GGAGGGCTCAGGATTTGAAGCAAGTGAAGACCCCTGGGACCAAGCTGCTAAAGTGCTAC 1640
QY 181 CCAGGGTGCAATACCTA 198
|||||
Db 1641 CCAGGGTGCAATACCTA 1658

RESULT 3
US-09-964-899-38
; Sequence 38, Application US/09964899
; Patent No. US2002017446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309

; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-964-899-38

Query Match 87.4%; Score 173; DB 9; Length 2404;
Best Local Similarity 92.4%; Pred. No. 1.6e-50;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
|||||
Db 827 TATGAAGCAGGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 886
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGA 120
|||||
Db 887 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGA 946
QY 121 GGAGGGCTCAGGATTTGAAGCAAGTGAAGACCCCTGGGACCAAGCTGCTAAAGTGCTAC 180
|||||
Db 947 GGAGGGCTCAGGATTTGAAGCAAGTGAAGACCCCTGGGACCAAGCTGCTAAAGTGCTAT 1006
QY 181 CCAGGGTGCAATACCT 197
|||||
Db 1007 CCAGGGTGCAATACCT 1023

RESULT 4
US-09-201-936-3
; Sequence 3, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/376,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-3

Query Match 87.4%; Score 173; DB 9; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.6e-50;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
|||||
Db 826 TATGAAGCAGGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGA 120

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Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGTCTTCACTGTGGA 945
QY 121 GGAGGCTCAGGATTTGAAGCAAGTGAAGACCCCTGGGACCAAGCATGCTTAAGTGTAC 180
Db 946 GGAGGGCTAAGTATTGAAGCCAGTGAAGACCCCTGGGAAACAACATGCTTAATGGTAT 1005
QY 181 CCAGGGTGCAAAATACCT 197
Db 1006 CCAGGGTGCAAAATATCT 1022

RESULT 5
US-09-974-592-3
; Sequence 3, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: 4623
; OTHER INFORMATION: n can be any nucleotide
; NAME/KEY: variation
; LOCATION: 4622
; OTHER INFORMATION: n can be any nucleotide
; US-09-974-592-3

Query Match 87.4%; Score 173; DB 10; Length 5232;
Best Local Similarity 92.4%; Pred. No. 2.2e-50;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATACACTAGTAAAGTGTCTTCACTGTGGA 60
Db 826 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATACACTAGTAAAGTGTCTTCACTGTGGA 885
QY 51 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAGTGAAGTGTCTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAGTGAAGTGTCTTCACTGTGGA 945
QY 121 GGAGGCTCAGGATTTGAAGCAAGTGAAGACCCCTGGGACCAAGCATGCTTAAGTGTAC 180
Db 946 GGAGGGCTAAGTATTGAAGCCAGTGAAGACCCCTGGGAAACAACATGCTTAATGGTAT 1005
QY 181 CCAGGGTGCAAAATACCT 197
Db 1006 CCAGGGTGCAAAATATCT 1022

RESULT 6
US-10-095-407-16/c
; Sequence 16, Application US/10095407
; Patent No. US20020164330A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/095,407
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/091,650
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
; US-10-095-407-16

Query Match 67.9%; Score 134.4; DB 9; Length 152331;
Best Local Similarity 83.2%; Pred. No. 3.6e-36;
Matches 164; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATACACTAGTAAAGTGTCTTCACTGTGGA 60
Db 3298 TATGAAGCAGCGATCGTTACTTTTGGATGCGATATATTCAGTTAAAGGAGCAGCTT 3239
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAGTGAAGTGTCTTCACTGTGGA 120
Db 3238 TCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAGTGAAGTGTCTTCACTGTGGA 3179
QY 121 GGAGGCTCAGGATTTGAAGCAAGTGAAGACCCCTGGGACCAAGCATGCTTAAGTGTAC 180
Db 3178 GGGGGCTAAGTATTGGGAAACCCACCGAA-AACCTTGGGACCAACATAATAATGGCAT 3120
QY 181 CCAGGGTGCAAAATACCT 197
Db 3119 CCAGGGTGTAATATCT 3103

RESULT 7
US-10-095-407-17
; Sequence 17, Application US/10095407
; Patent No. US20020164330A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/095,407
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/091,650
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
; US-10-095-407-17

Query Match 55.4%; Score 109.6; DB 9; Length 176373;
Best Local Similarity 86.4%; Pred. No. 2e-27;
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	Matches	121;	Conservative	0;	Mismatches	19;	Indels	0;	Gaps	0;
QY	58	CTTCAAGAGCTGATTTTATGCTTTTAGTGAAAGCGCATAAAGTGAAGTCGTCCACTGT	117							
Dd	12549	CTTTCAGAAGCTGGATTTTATGCTTTTAGTGAAAGTGATAAAGTAAAGTGCTTTCACTGT	12608							
QY	118	GGAGGAGGGGTCACGGATTGGAAGCACAAGTAAGACCCTTGGGACCAGCATGCCTAAGTGC	177							
Dd	12609	GGAGGGGGCTACTGATTGGAAGCCCAGGAGCACCTTGGGAACAACATGATAATGG	12668							
QY	178	TACCCAGGGTGCAAATACCT	197							
Dd	12669	CATCAGGGTGTAATATCT	12688							

```

RESULT 8
US-09-201-936-5
; Sequence 5, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2470)...(2470)
; OTHER INFORMATION: N may be any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2476)...(2476)
; OTHER INFORMATION: N may be any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2483)...(2483)
; OTHER INFORMATION: N may be any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2602)...(2602)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-5

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QY   162 CCAGCATGCTAAAGTGTACCCAGGGTGCAAAATACCT 197
      || ||||| ||||| || ||||| || ||||| || |||||
Db   1118 TCACATGCCAAGTGGTTTCCAAGGTGTGAGTACTT 1153
      || ||||| ||||| || ||||| || ||||| || |||||

RESULT 9
US-09-954-531-16
; Sequence 16, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 3076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-16

Query Match          38.4%; Score 76; DB 9;
Best Local Similarity 67.9%; Pred. No. 2e-16;
Matches 106; Conservative 0; Mismatches 5

QY   42 AGTTAACAGGACAGCTTCAGAGCTGCATTATATGCTTT
      || ||||| ||||| ||||| ||||| || ||||| || |||||
Db   1534 AGTTAATCCGAGCAGCTTCGAAGTCGGGTTTTATATATG
      || ||||| ||||| ||||| ||||| || ||||| || |||||

QY   102 GAAGTCGCTTCACCTGTGGAGGAGGGCTCACCGATTTGGAAGC
      || ||||| ||||| ||||| ||||| || ||||| || |||||
Db   1594 CAATAGCTTTTGCCTGATGTGGACTCAGGTGTGGGAAT
      || ||||| ||||| ||||| ||||| || ||||| || |||||

QY   162 CCAGCATGCTAAAGTGTACCCAGGGTGCAAAATACCT 197
      || ||||| ||||| || ||||| || ||||| || |||||
Db   1654 TCACATGCCAAGTGGTTTCCAAGGTGTGAGTACTT 1689
      || ||||| ||||| || ||||| || ||||| || |||||

```

RESULT 10
US-09-954-456-1635
; Sequence 1635, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638

[illegible]

Query Match 34.3%; Score 68; DB 10; Length 2676;
Best Local Similarity 64.7%; Pred. No. 1.2e-13;
Matches 101; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 42 AGTTACAGGAGCAGCTGCGAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGT 101
DB 1106 AGTTATCCAGGAGCTTGCAGTGGCGCTTTTATTATACAGACACAGTGATGATGT 1165
QY 102 GAAGTCTTCCACTGTGGAGGAGGCTCAGCGATTGGAGGCCAAGTGAAGACCCCTGGGA 161
DB 1166 CAAAGTCTTCTGTGTGGTGGCTGAGGTGGGAATCTGGAGATGACCCCTGGGT 1225
QY 162 CCAGCATGCTAAGTCTACCCAGGCTGCAAAATACCT 197
DB 1225 GGAACATGCCAAGTGGTTTCCCAAGTGTGAGTACTT 1261

RESULT 14
US-09-201-936-7
; Sequence 7, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version: 3.0
; SEQ ID NO 7
; LENGTH: 2580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2412)...(2412)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-7

Query Match 33.2%; Score 65.8; DB 9; Length 2580;
Best Local Similarity 60.2%; Pred. No. 7e-13;
Matches 109; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 17 TTATGTTTGGACATGATATACCTAGTTTAAAGAGGAGCTTGAAGAGCTGGATTTT 76
DB 1064 TTATGTTTGGACATGATATACCTAGTTTAAAGAGGAGCTTGAAGAGCTGGATTTT 1123

QY 77 ATGCTTTAGGTGAAGCGGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 136
DB 1124 ATTATGTGGTGGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1183
QY 137 GGAAGCCCAAGTGAAGACCCCTGGACCATGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 196
DB 1184 GGAATCTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1243
QY 197 T 197
DB 1244 T 1244

RESULT 15
US-09-880-107-3354
; Sequence 3354, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3354
; LENGTH: 3532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 037547
US-09-880-107-3354

Query Match 33.2%; Score 65.8; DB 10; Length 3532;
Best Local Similarity 60.2%; Pred. No. 8.1e-13;
Matches 109; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 17 TTACTTTTGAACATGATATACCTAGTTTAAAGAGGAGCTTGAAGAGCTGGATTTT 76
DB 1986 TTATGTTTGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2045
QY 77 ATGCTTTAGGTGAAGCGGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 136
DB 2046 ATTATGTGGTGGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2105
QY 137 GGAAGCCCAAGTGAAGACCCCTGGACCATGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 196
DB 2106 GGAATCTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2165
QY 197 T 197
DB 2166 T 2166

Search completed: April 19, 2003, 03:05:22
Job time : 148 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2003, 01:38:31 ; Search time 1057 Seconds
(without alignments)
3033.781 Million cell updates/sec

Title: US-09-654-743-51

Perfect score: 198

Sequence: 1 tatgaagcagcagtcgttac.....accacgggtgcaataaccta 198

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estor:*
5: em_estov:*
6: em_estpi:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
C 1	168	84.8	628	9	AI573382
C 2	108	54.5	617	10	BB663325
C 3	103.4	52.2	504	10	BB650856
C 4	100.8	50.9	318	12	BF659610
C 5	98	49.5	566	13	BM220130
C 6	98	49.5	584	14	BQ552032
					BQ552032 H4013A06-

7	92.2	46.6	1177	14	BM805359
8	90.2	45.6	536	9	AUI23207
9	84.2	42.5	716	10	AV706807
10	76	38.4	341	10	AW375598
11	76	38.4	354	10	AW375594
12	76	38.4	402	10	AW846507
13	76	38.4	531	10	AW375599
14	76	38.4	532	10	AW846525
15	76	38.4	546	10	AW846421
16	76	38.4	571	10	AW375649
17	76	38.4	582	10	AW846337
18	76	38.4	590	10	BE268377
19	76	38.4	621	10	AW375648
20	76	38.4	680	10	AW375625
21	76	38.4	886	14	BQ652590
22	75.2	38.0	269	10	BE506790
23	69.2	34.9	567	13	BI961039
24	68.4	34.5	420	17	AQ011995
25	68	34.3	323	12	BE847058
26	68	34.3	385	12	BE851680
27	66	34.3	557	9	AA197349
28	66	33.3	673	13	BJ045197
29	65.8	33.2	441	13	BM312708
30	65.8	33.2	563	9	AA702174
31	65.8	33.2	552	10	AV704923
32	65.8	33.2	851	13	BI253303
33	65.8	33.2	896	14	BQ439248
34	65.4	33.0	354	9	AA354707
35	64.2	32.4	506	13	BM126304
36	63.8	32.2	889	14	BQ720079
37	62.6	31.6	780	13	BI771720
38	62.4	31.5	302	14	R83677
39	62.4	31.5	512	13	BI326908
40	62.4	31.5	584	10	AW375608
41	62.4	31.5	645	10	AW375611
42	61.2	30.9	620	13	BM494270
43	61	30.8	288	12	BF016190
44	60.6	30.6	395	9	AI552965
45	59.6	30.1	423	12	BF325539

ALIGNMENTS

RESULT 1

AI573382/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AI573382 628 bp mRNA linear EST 16-APR-1999
mn83e12.x1 Stratiogene mouse Tcell 937311 Mus musculus CDNA clone
IMAGE:550702 3' similar to TR:Q60989 Q60989 MIHA. ; mRNA sequence.

AI573382.1 GI:4536756

EST.

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 628)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter

, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LINL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: similarity on wrong strand

BM805359 AGENCOURT
AUI23207 AUI23207
AW375598 QVO-CT017
AW375594 QVO-CT017
AW846507 QVO-CT017
AW375599 QVO-CT017
AW846421 QVO-CT017
AW375649 QVO-CT017
AW846337 QVO-CT017
BE268377 601124994
AW375648 QVO-CT017
AW375625 QVO-CT017
BQ652590 AGENCOURT
BE506790 db87908.Y
BI961039 MONOL_5.C
AQ011995 HS_2190_A
BE847058 uw23406.Y
BE851680 uw99807.Y
AA197349 mu21c08.Y
BJ045197 BJ045197
BM312708 lg78a10.Y
AA702174 z191908.S
AV704923 AV704923
BI253303 602973538
BQ439248 AGENCOURT
AA354707 EST63004
BM126304 lf04609.Y
BQ720079 AGENCOURT
BI771720 603058472
R83677 yp16f10.r1
BI326908 AR071E101
AW375608 QVO-CT017
AW375611 QVO-CT017
BM494270 IPCGBrl_1
BF016190 uy32a08.Y
AI552965 vg63h10.Y
BF325539 CMO-AN000

Best Local Similarity 93.8%; Pred. No. 6.7e-22;
Matches 105; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 53 AGCAGCTTCAGAGCTGATTTATGCTTTAGGTGAAGCGCATAAAGTGAAGTCTTCC 112
DB 317 AGCAGCTTCAGAGCTGATTTATGCTTTAGGTGAAGCGCATAAAGTGAAGTCTTCC 258
QY 113 ACTGTGGAGGAGGCTCAGGATTCGAGCCCAAGTGAAGACCCCTGGGACCA 164
DB 257 ACTGTGGAGGAGGCTCAGGATTCGAGCCCAAGTGAAGACCCCTGGGACCA 206

RESULT 5
LOCUS BM220130/c 566 bp mRNA linear EST 31-JAN-2002
DEFINITION C0935E08-3 NIA Mouse 12.5-dpc Male Genital Ridge/Mesonephros cDNA
Library (Long) Mus musculus cDNA clone C0935E08 3', mRNA sequence.

ACCESSION BM220130
VERSION BM220130.1 GI:17780130
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 566)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Pantano, S., Luo, A.
and Ko, M.S.H.

TITLE Systematic Analyses of NIA Mouse 12.5-dpc Male Genital
Ridge/Mesonephros cDNA Library (Long)
JOURNAL Unpublished (2001)
COMMENT Laboratory of Genetics

National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: C0935 row: E column: 08
Seq primer: -21M13 Forward
High quality sequence stop: 566
POLYA=Yes.

FEATURES Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="niaEST:C0935E08-3"
/db_xref="taxon:10090"
/clone="C0935E08"
/clone_lib="NIA Mouse 12.5-dpc Male Genital
Ridge/Mesonephros cDNA Library (Long)"
/sex="Male"
/tissue_type="Male genital ridge/mesonephros"
/dev_stage="12.5-dpc"
/lab_host="DH10B"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Double-stranded
cDNAs were synthesized with an Oligo(dT) primer
[Invitrogen]:
5'-pCAGTGTCTAGTACGCGAGCGCGCCCTTTTCTTTT-3' from
1.8 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lona-linker LL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.4 kb. The library was constructed

BASE COUNT 183 a 123 c 84 g 176 t
ORIGIN by Yulan Piao (NIA)."

Query Match 49.5%; Score 98; DB 13; Length 566;
Best Local Similarity 95.3%; Pred. No. 7.9e-21;
Matches 101; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 82 TTAGTGAAGCGCATAAAGTGAAGTCTTCCACTGTGGAGGAGGCTCAGGATTGGAAG 141
DB 260 TTAGTGAAGCGCATAAAGTGAAGTCTTCCACTGTGGAGGAGGCTCAGGATTGGAAG 201

QY 142 CCAAGTGAAGACCCCTGGGACCAAGTGAAGTCTTCCACTGTGGAGGAGGCTCAGGATTGGAAG 187
DB 200 CCAAGTGAAGACCCCTGGGACCAAGTGAAGTCTTCCACTGTGGAGGAGGCTCAGGATTGGAAG 155

RESULT 6
LOCUS BQ552032/c 584 bp mRNA linear EST 20-JUN-2002
DEFINITION H4013A06-3 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
H4013A06 3', mRNA sequence.

ACCESSION BQ552032
VERSION BQ552032.1 GI:21452918
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 584)
VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Martin,
P.R., Staggs, C.A., Bassey, U., Alaba, K., Hamatani, T., Kargul, G.J.,
Luo, A.G. and Ko, M.S.H.

TITLE Assembly, verification, and initial annotation of NIA 7.4K mouse
cDNA clone set
JOURNAL Unpublished (2002)
COMMENT Other_ESTs: H4013A06-5
Contact: Yong Qian
Laboratory of Genetics

National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://igsun.grc.nia.nih.gov/cDNA/NIA_7.4k.html for details.
Plate: H4013 row: A column: 06
Seq primer: -21M13 Forward
High quality sequence stop: 584
POLYA=Yes.

FEATURES Location/Qualifiers
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/strain="C57BL/6"
/db_xref="niaEST:H4013A06-3"
/db_xref="taxon:10090"
/clone="H4013A06"
/clone_lib="NIA Mouse 7.4K cDNA Clone Set"
/sex="mixed"
/dev_stage="mixed"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
clone is among a rearrayed set of 7,407 clones from more
than 20 cDNA libraries."
BASE COUNT 189 a 125 c 86 g 184 t
ORIGIN

Query Match 49.5%; Score 98; DB 14; Length 584;
Best Local Similarity 95.3%; Pred. No. 8.1e-21;
Matches 101; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 82 TTAGTGAAGCGCATAAAGTGAAGTCTTCCACTGTGGAGGAGGCTCAGGATTGGAAG 141
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADBCOF01"
/clone_lib="ADB"
/tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"
/note="vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 207 a 148 c 193 g 163 t 5 others
ORIGIN

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Best Local Similarity 84.1%; Pred. No. 2.8e-16;
Matches 95; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 85 GGTGAAGCGGATAAGTGAAGTGTCTTCACTGTGGAGAGGGCTCAGCGATTGGAGCCCA 144
Db 156 GGTGAAGGTGATAAGTAAAGTGTCTTCACTGTGGAGAGGGCTTAACTGATTGGAAGCCC 215

QY 145 AGTGAAGACCCCTGGGACCAAGCATGTAAAGTGTACCCAGGGTCAAAATACCT 197
Db 216 AGTGAAGACCCCTGGGAACAACATGCTAAATGGTATCCAGGGTAAAGAACTACT 268

RESULT 10
AW375598
LOCUS QV0-CT0179-300999-024-f08 CT0179 Homo sapiens cDNA, mRNA linear EST 04-FEB-2000
DEFINITION The FAPESP/LICR Human Cancer Genome Project
ACCESSION AW375598
VERSION AW375598.1 GI:6880161
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 341)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV0st2-QV0-CT0179-
300999-024-f08st3-1999-09-30st4-1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 341.
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="CT0179"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 91 a 70 c 83 g 97 t
ORIGIN

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Best Local Similarity 67.9%; Pred. No. 7.9e-14;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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Db 80 AGTTAACTCTGAGCAGCTTGAAGTGGGGTTTTTATTATGTGGGTAAACAGTGATGATG 139

QY 102 GAAGTGTCTTCCACTGTGAGAGGGCTCAGGATTGGAAGCCCAAGTGAAGACCCCTGGGA 161
Db 140 CAAATGCTTTTGTGTGATGTGGAGCTCAGGTGTGGGAATCTGGAGATGATCCATGGT 199

QY 162 CCAGCATGTCTAAGTGTACCCAGGGTCAAAATACCT 197
Db 200 TCACATGCCAAGTGGTTCACAGGTGTGAGTACTT 235

RESULT 11
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LOCUS QV0-CT0179-300999-024-d06 CT0179 Homo sapiens cDNA, mRNA linear EST 04-FEB-2000
DEFINITION The FAPESP/LICR Human Cancer Genome Project
ACCESSION AW375594
VERSION AW375594.1 GI:6880157
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 354)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV0st2-QV0-CT0179-
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High quality sequence start: 12
High quality sequence stop: 354.
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Location/Qualifiers
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/clone_lib="CT0179"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 96 a 73 c 86 g 99 t
ORIGIN

Query Match 38.4%; Score 76; DB 10; Length 354;
Best Local Similarity 67.9%; Pred. No. 7.9e-14;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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Db 93 AGTTAACTCTGAGCAGCTTGAAGTGGGGTTTTTATTATGTGGGTAAACAGTGATGATG 152

QY 102 GAAGTGTCTTCCACTGTGAGAGGGCTCAGGATTGGAAGCCCAAGTGAAGACCCCTGGGA 161
Db 153 CAAATGCTTTTGTGTGATGTGGAGCTCAGGTGTGGGAATCTGGAGATGATCCATGGT 212
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SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS 1. (bases 1 to 532)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.J.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV0-CT0179-070
300-143-0046t3-2000-03-07&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 4

High quality sequence stop: 531.

Location/Qualifiers

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="CT0179"

/dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:

SmaI; A mini-library was made by cloning products derived

from ORSTES PCR (U.S. Letters Patent application No. 196

,716 - Ludwig Institute for Cancer Research) profiles

into the PUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

BASE COUNT 160 a 107 c 122 g 143 t

ORIGIN

Query Match 38.4%; Score 76; DB 10; Length 532;

Best Local Similarity 67.9%; Pred. No. 1e-13;

Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTACAGGAGCAGCTTGCAGAGCTGGATTATGCTTTAGTGAAGCGGATAAGT 101

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 96 AGTTAATCTGTGACAGCTTGCAGAGCTGGATTATGCTTTAGTGAAGCGGATAAGT 155

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 102 GAAGTGCTCCACTGTGAGAGGCTCAGGATGGAGCCAAAGTGAAGACCCCTGGGA 161

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 156 CAATGCTTTGCTGTGATGTGGACTCAGGTGTGGAACTCGAGATGATCATGGGT 215

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QY 162 CCAGCATGCTAAGTGTCTACCCAGGCTGCAAACTCT 197

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 216 TCAACATGCCAAGTGGTTTCCAAAGGTGTGAGTACTT 251

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15

AW846421

LOCUS 546 bp mRNA linear EST 19-MAY-2000

DEFINITION QV0-CT0179-070300-143-a04 CT0179 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW846421

VERSION AW846421.1 GI:7941938

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1. (bases 1 to 546)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT

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Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV0-CT0179-070
300-143-0046t3-2000-03-07&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 6

High quality sequence stop: 546.

Location/Qualifiers

1. .546

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="CT0179"

/dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:

SmaI; A mini-library was made by cloning products derived

from ORSTES PCR (U.S. Letters Patent application No. 196

,716 - Ludwig Institute for Cancer Research) profiles

into the PUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

BASE COUNT 169 a 106 c 123 g 148 t

ORIGIN

Query Match 38.4%; Score 76; DB 10; Length 546;

Best Local Similarity 67.9%; Pred. No. 1.1e-13;

Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTACAGGAGCAGCTTCCAAGAGCTGGATTATGCTTTAGTGAAGCGGATAAGT 101

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Db 121 AGTTAATCTGTGACAGCTTCCAAGAGCTGGATTATGCTTTAGTGAAGCGGATAAGT 180

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QY 102 GAAGTGCTCCACTGTGAGAGGCTCAGGATGGAGCCAAAGTGAAGACCCCTGGGA 161

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Db 181 CAATGCTTTGCTGTGATGTGGACTCAGGTGTGGAACTCGAGATGATCATGGGT 240

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 162 CCAGCATGCTAAGTGTCTACCCAGGCTGCAAACTCT 197

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Db 241 TCAACATGCCAAGTGGTTTCCAAAGGTGTGAGTACTT 276

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Search completed: April 19, 2003, 02:27:11

Job time : 1062 secs



Creation date: 11-28-2003
Indexing Officer: DSANFORD - DEBRA SANFORD
Team: OIPEBackFileIndexing
Dossier: 09654743

Legal Date: 05-01-2003

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